



Replacement Sheet

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FIGURE 6A

Numbering is according to Kimura et al.

1. 'A' Allele, CYP2D6*3, A2637 deletion. Frameshift resulting in zero enzyme activity

2637

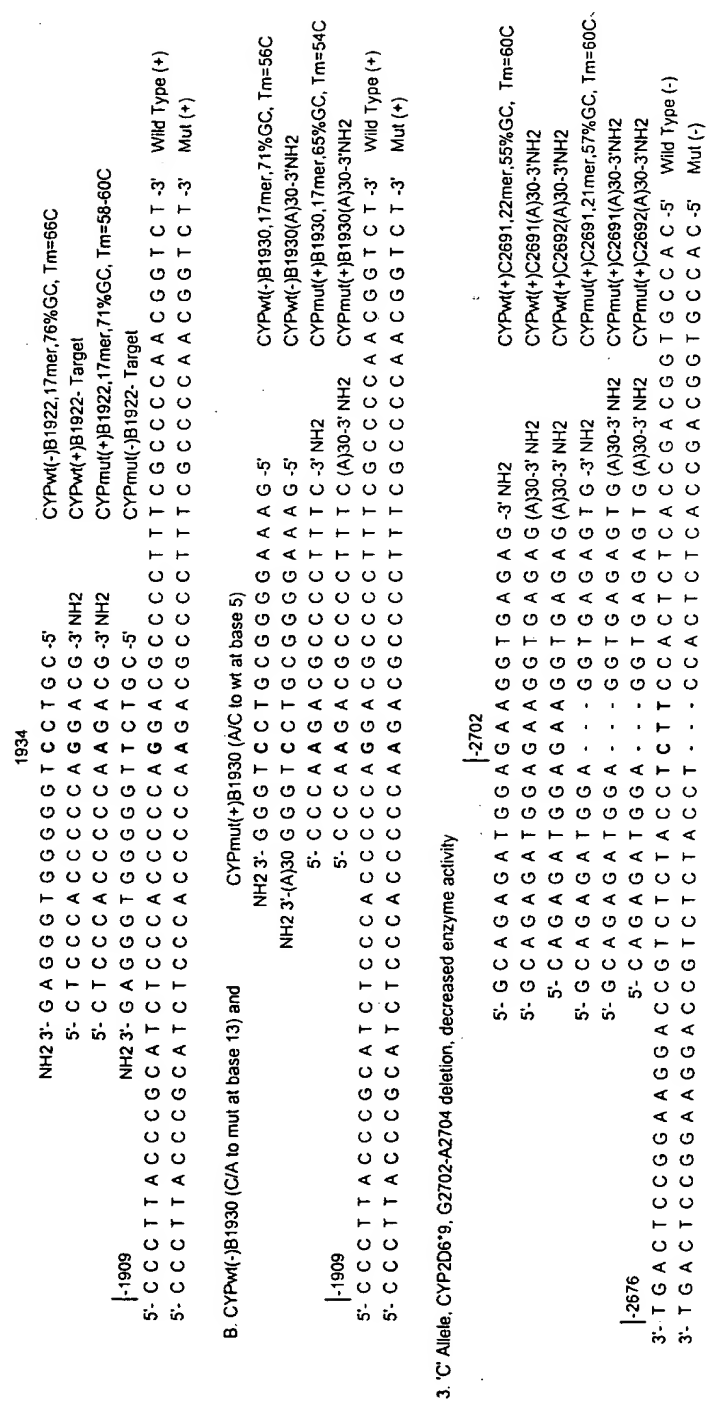
5'-GCTA A C T G A G C A C A G G A T G A C C -3' NH2	CYPwt(+)/A2624, 22mer, 54%GC, Tm=63-64C
5'-GCTA A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)/A2624(A)30-3'NH2
5'-CTA A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)/A2625(A)30-3'NH2
5'-CTA A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)/A2625b(A)30-3'NH2
5'-GCTA A C T G A G C A C A G G A T G A (A)30-3' NH2	CYPwt(+)/A2625c(A)30-3'NH2
5'-GCTA A C T G A G C A C - G G A T G A C C -3' NH2	CYPmut(+)/A2624, 21mer, 57%GC, Tm=61-63C
5'-GCTA A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)/A2624(A)30-3'NH2
5'-CTA A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)/A2625(A)30-3'NH2
5'-CTA A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)/A2625b(A)30-3'NH2
5'-CTA A C T G A G C A C - G G A T G A (A)30-3' NH2	CYPmut(+)/A2625c(A)30-3'NH2
5'-g c t a a c l g a g c a c a g g a l g (A)30-3' NH2	CYPwt(+)/A2624b(A)30-3'NH2
NH2 3'-(A)30 g a l l g a c t c g l g t c c t a c l g -5'	CYPwt(-)/A2625(A)30-3'NH2
x= 2-Amino-dA	CYPwt(+)/2629a(A)30-3'NH2
x= C-5 propynyl-C	CYPwt(+)/2629b(A)30-3'NH2
x= C-5 propynyl-C	CYPwt(+)/2629c(A)30-3'NH2
5'-GCTGGATGAGCTGCTA A C T G A G C A C A G G A T G A C C T G G G A C C C A G C C C -3'	Wild Type (+)
5'-GCTGGATGAGCTGCTA A C T G A G C A C - G G A T G A C C T G G G A C C C A G C C C -3'	Mut (+)



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FIGURE 6B

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FIGURE 6C

4. 'E' Allele, CYP2D6*7, A3023C, H324P amino acid change results in zero enzyme activity

A. wt Probe - CYPwt(-)E3009 (T/C to mut at base 5) & CYPmut(+E3009 (C/A to wt at base 15)

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NH2 3'- C G A G T A C T A G G A T G T A G G C C -5'
NH2 3'-(A)30 C G A G T A C T A G G A T G T A G G C C -5'
5'- G C T C A T G A T C C T A C C T C C G -3' NH2
5'- G C T C A T G A T C C T A C C T C C G (A)30-3' NH2
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G A T G T G C A G C
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G A T G T G C A G C
| -2998
CYPwt(-)E3009, 19mer, 53%GC, Pred Tm=57
CYPwt(-)E3009(A)30-3'NH2
CYPmut(+E3009, 19mer, 58%GC, Pred Tm=59C
CYPmut(+E3009(A)30-3'NH2
G T G A G C C C A T C -3' Wild Type (+)
G T G A G C C C A T C -3' Mut (+)
-3038-Intron Start
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B. CYPwt(-)E3018 (T/C to mut at base 14) and

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NH2 3'- G G A T G T A G G C C T A C A C G T C -5'
NH2 3'-(A)30 C C T A C A T C C G G A T G T G C A G -3'
5'- C C T A C C T C C G G A T G T G C A G -3' NH2
5'- C C T A C C T C C G G A T G T G C A G -3' NH2
3'- G G A T G G A G G C C T A C A C G T C -5'
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G A T G T G C A G C
5'- T G G G G C C T C C T G C T C A T G A T C C T A C C T C C G A T G T G C A G C
| -2998
CYPwt(+E3018 (C/T to wt at base 6)
CYPwt(-)E3018, 19mer, 58%GC, Tm=60
CYPwt(+E3018- Target
CYPmut(+E3018, 19mer, 63%GC, Tm=62C
CYPmut(-)E3018- Target
G T G A G C C C A T C -3' Wild Type (+)
G T G A G C C C A T C -3' Mut (+)
-3038-Intron Start
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5. 'G' Allele, CYP2D6*8, G1846T, Stop codon, zero enzyme activity

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NH2 3'- C A C T C C G G T G G G T G A T G G (A)30-3' NH2
NH2 3'-(A)30 G T G A G G C C A C C C A C C -5'
5'- C A C T C C T G T G G G T G A T G G (A)30-3' NH2
5'- C A C T C C T G T G G G T G A T G G G C A G A A G G G C A C A A G C G G G -3'
5'- G T G C C G C C T T C G C C A C T C C T G T G G G T G A T G G G C A G A A G G G C A C A A G C G G G -3'
Exon 3 end -1846
CYPwt(+G1840(A)30-3'NH2, 18mer, 67%GC, Tm=60
CYPwt(-)G1840(A)30-3'NH2
CYPmut(+G1840(A)30-3'NH2, 18mer, 61%GC, Tm=57
CYPmut(-)G1840(A)30-3'NH2
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FIGURE 6D

6. 'T' Allele, CYP2D6*6, T1795 deletion, Frameshift resulting in zero enzyme activity

5'- G C T G G A G C A G T G G G T G A C -3' NH2
5'- G C T G G A G C A G T G G G T G A C (A)30-3' NH2
5'- C T G G A G C A G T G G G T G A C (A)30-3' NH2
5'- G C T G G A G C A G - G G G T G A C -3' NH2
5'- G C T G G A G C A G - G G G T G A C (A)30-3' NH2
5'- C T G G A G C A G - G G G T G A C (A)30-3' NH2
5'- G G G C A A G A A G T C G C T G G A G C A G T G G G T G A C C G A G G A G G C C G C C T G C C T -3' Wild Type (+)
5'- G G G C A A G A A G T C G C T G G A G C A G - G G G T G A C C G A G G C C G C C T G C C T -3' Mut (+)

7. 2D6/2D7/2D8 Controls - The 2D6/7/8 probes were designed in the 1600 region of the 2D6 gene. The purpose of the designs was to find region somewhere between the PCR primers were it would be easy to discriminate between 2D6 and its two pseudogenes, 2D7 and 2D8. The purpose of the designs is to demonstrate that the PCR amplicon is from the 2D6 gene, not one of the pseudogenes.

1603- |
5'- G A C C A G G G G A G C - A T A G G (A)30-3' NH2
5'- G A C C T T G T G G A G C G C C A G (A)30-3' NH2
5'- G A C C A G G A A A G C - A C A G G (A)30-3' NH2
5'- G A C C A G G A A A G C - A C A G G (A)30-3' NH2
5'- G G G A G A C C A G G G A G C - A T A G G T T G G A G T G G G T G G T -3' 2D6 (+)
5'- G G G A G A C C T T G T G G A G C G C C A G G T T G G A G T G G G T G G C -3' 2D7 (+)
5'- G G G A G A C C A G G A A A G C - A C A G G T T G G A G T G G G C G C -3' 2D8 (+)

8. Pos/Neg Control probes- These probes were designed as true positive and negative control probes. They consist of the same semi-random sequence, with the positive control probe having a 5' Biotin.

5' Biotin- A T C A T T C C A A T C A T C C A T A T C A T C (A)25-3' NH2
5'- A T C A T T C C A A T C A T C C A T A T C A T C (A)25-3' NH2
CYP(+)/ran(A)25-5' Biotin.3' NH2
CYP(+)/ran(A)25-3' NH2